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SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 3-6-07
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 10/636,065
Location (Bldg/Room#): 2A59 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Antisense LAP oligos
Inventors (please provide full names): R G KORNELUK et al.

Earliest Priority Date: 8-7-03

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

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- EXACT IDENTITY needed
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____ AA Sequence (#)

____ Structure (#)

____ Bibliographic

____ Litigation

____ Fulltext

____ Other

Vendors and cost where applicable

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____ Westlaw _____ WWW/Internet

____ In-house sequence systems

____ Commercial _____ Oligomer _____ Score/Length

____ Interference _____ SPDI _____ Encode/Transl

____ Other (specify)

SCORE Search Results Details for Application 10636065 and Search Result 20060809_170457_us-10-636-065-22.max.rge.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10636065 and Search Result 20060809_170457_us-10-636-065-22.max.rge.

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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 07:08:17 ; Search time 981 Seconds
(without alignments)
1238.533 Million cell updates/sec

Title: US-10-636-065-22
Perfect score: 19
Sequence: 1 atcttctcttgaaaatagg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 2541152

Minimum DB seq length: 0
Maximum DB seq length: 70

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : GenEmbl:*

- 1: gb_env:*
- 2: gb_pat:*
- 3: gb_ph:*
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- 12: gb_htg:*
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- 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match Length	DB	ID	Description
	1	19	100.0	19	2	AR451377 Sequence
	2	19	100.0	19	2	AX411922 Sequence
	3	19	100.0	20	2	AR103291 Sequence
	4	19	100.0	33	2	CQ890068 Sequence
c	5	18	94.7	19	2	CS027754 Sequence
	6	18	94.7	19	2	CS028221 Sequence
	7	18	94.7	20	2	AR103290 Sequence
	8	17	89.5	20	2	AR103292 Sequence
	9	15.8	83.2	50	2	AR688306 Sequence
	10	15	78.9	20	2	AR103293 Sequence
c	11	14.8	77.9	47	2	CS249356 Sequence
	12	14.6	76.8	47	2	AR290347 Sequence
c	13	14.4	75.8	60	2	CQ550497 Sequence
c	14	14.2	74.7	47	2	CS249313 Sequence
	15	14.2	74.7	60	2	CQ544851 Sequence
	16	14.2	74.7	69	2	A42870 Sequence 2
	17	14.2	74.7	69	2	AR271404 Sequence
c	18	14	73.7	47	2	CS174292 Sequence
c	19	14	73.7	51	2	CS174290 Sequence
	20	14	73.7	51	2	CS174291 Sequence
c	21	14	73.7	60	2	CQ550203 Sequence
	22	13.8	72.6	41	2	AX516067 Sequence
	23	13.8	72.6	41	2	AX517473 Sequence
	24	13.8	72.6	41	2	AX520878 Sequence
	25	13.8	72.6	47	2	AR290700 Sequence
c	26	13.8	72.6	51	2	CS048040 Sequence
	27	13.8	72.6	51	2	CS048041 Sequence
	28	13.8	72.6	54	2	AR018139 Sequence
	29	13.8	72.6	54	2	AR152321 Sequence
	30	13.8	72.6	54	2	I71050 Sequence 1
c	31	13.4	70.5	17	2	BD259661 Regulatio
c	32	13.4	70.5	47	2	CS249371 Sequence
c	33	13.4	70.5	50	2	CQ813869 Sequence
c	34	13.4	70.5	52	2	CS185025 Sequence
	35	13.4	70.5	57	2	CS185026 Sequence
c	36	13.4	70.5	63	2	CS248789 Sequence
c	37	13.2	69.5	30	2	AX925500 Sequence
	38	13.2	69.5	40	2	AR089811 Sequence
	39	13.2	69.5	45	2	AX299290 Sequence
c	40	13.2	69.5	51	2	CQ007549 Sequence
c	41	13.2	69.5	51	2	AX164960 Sequence
c	42	13.2	69.5	60	2	CQ539698 Sequence
c	43	13.2	69.5	65	2	CQ533891 Sequence
	44	13.2	69.5	65	2	CQ534999 Sequence
	45	13	68.4	20	2	AR103294 Sequence
c	46	13	68.4	47	2	CS249333 Sequence
c	47	13	68.4	47	2	CS249416 Sequence
c	48	13	68.4	51	2	CQ786939 Sequence
	49	13	68.4	51	2	CQ786940 Sequence
c	50	13	68.4	64	2	CS243271 Sequence
	51	13	68.4	64	2	CS243272 Sequence

52	12.8	67.4	17	2	AX723981	AX723981 Sequence
53	12.8	67.4	18	2	AX019204	AX019204 Sequence
c 54	12.8	67.4	28	2	AR139423	AR139423 Sequence
c 55	12.8	67.4	28	2	AR595251	AR595251 Sequence
c 56	12.8	67.4	29	2	CQ867394	CQ867394 Sequence
c 57	12.8	67.4	35	2	BD107810	BD107810 Opsonic a
c 58	12.8	67.4	35	2	AR381833	AR381833 Sequence
c 59	12.8	67.4	35	2	AR715212	AR715212 Sequence
c 60	12.8	67.4	39	2	BD093203	BD093203 Useful po
c 61	12.8	67.4	39	2	BD142368	BD142368 Novel pol
c 62	12.8	67.4	39	2	E36089	E36089 Novel polyp
c 63	12.8	67.4	39	2	AR219208	AR219208 Sequence
c 64	12.8	67.4	39	2	AR367381	AR367381 Sequence
c 65	12.8	67.4	40	2	A99037	A99037 Sequence 45
66	12.8	67.4	40	2	A99040	A99040 Sequence 48
67	12.8	67.4	40	2	BD093206	BD093206 Useful po
68	12.8	67.4	40	2	BD142371	BD142371 Novel pol
69	12.8	67.4	40	2	E36092	E36092 Novel polyp
c 70	12.8	67.4	40	2	AR195354	AR195354 Sequence
71	12.8	67.4	40	2	AR195357	AR195357 Sequence
72	12.8	67.4	40	2	AR219211	AR219211 Sequence
c 73	12.8	67.4	40	2	AR615390	AR615390 Sequence
74	12.8	67.4	40	2	AR615393	AR615393 Sequence
c 75	12.8	67.4	41	2	AR481811	AR481811 Sequence
76	12.8	67.4	41	2	AX516294	AX516294 Sequence
77	12.8	67.4	41	2	AX518690	AX518690 Sequence
c 78	12.8	67.4	47	2	CS174347	CS174347 Sequence
c 79	12.8	67.4	47	2	AR289557	AR289557 Sequence
c 80	12.8	67.4	48	2	A51850	A51850 Sequence 14
c 81	12.8	67.4	48	2	AR085823	AR085823 Sequence
c 82	12.8	67.4	51	2	CQ005311	CQ005311 Sequence
c 83	12.8	67.4	51	2	CQ875030	CQ875030 Sequence
c 84	12.8	67.4	51	2	CS174345	CS174345 Sequence
85	12.8	67.4	51	2	CS174346	CS174346 Sequence
86	12.8	67.4	51	2	AX115597	AX115597 Sequence
c 87	12.8	67.4	55	2	CQ756599	CQ756599 Sequence
88	12.8	67.4	55	2	CQ756600	CQ756600 Sequence
c 89	12.8	67.4	55	2	CQ756679	CQ756679 Sequence
90	12.8	67.4	55	2	CQ756680	CQ756680 Sequence
c 91	12.8	67.4	55	2	CQ874997	CQ874997 Sequence
92	12.8	67.4	55	2	CQ874998	CQ874998 Sequence
c 93	12.8	67.4	58	2	AX927318	AX927318 Sequence
c 94	12.8	67.4	58	4	AJ718126	AJ718126 Nicotiana
95	12.8	67.4	60	2	CQ542491	CQ542491 Sequence
c 96	12.8	67.4	60	2	CQ543554	CQ543554 Sequence
c 97	12.8	67.4	60	2	CQ548974	CQ548974 Sequence
c 98	12.8	67.4	62	2	AX428426	AX428426 Sequence
c 99	12.8	67.4	64	2	CS060522	CS060522 Sequence
100	12.8	67.4	64	2	CS060523	CS060523 Sequence

ALIGNMENTS

RESULT 1

AR451377

LOCUS AR451377 19 bp DNA linear PAT 20-FEB-2004

DEFINITION Sequence 22 from patent US 6673917.

ACCESSION AR451377

VERSION AR451377.1 GI:42682402

KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Korneluk,R.G., LaCasse,E., Baird,S., Holcik,M. and Young,S.
TITLE Antisense IAP nucleic acids and uses thereof
JOURNAL Patent: US 6673917-A 22 06-JAN-2004;
University of Ottawa; Ottawa;
CAX;

FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCTTCTCTTGAAAATAGG 19
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Db 1 ATCTTCTCTTGAAAATAGG 19

RESULT 2

AX411922

LOCUS AX411922 19 bp DNA linear PAT 14-JUN-2002

DEFINITION Sequence 22 from Patent WO0226968.

ACCESSION AX411922

VERSION AX411922.1 GI:21444387

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE 1

AUTHORS Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.

TITLE Antisense iap nucleic acids and uses thereof

JOURNAL Patent: WO 0226968-A 22 04-APR-2002;

University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)

FEATURES Location/Qualifiers

source 1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="based on Homo sapiens"

ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCTTCTCTTGAAAATAGG 19
|||||
Db 1 ATCTTCTCTTGAAAATAGG 19

RESULT 3

AR103291

LOCUS AR103291 20 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 11 from patent US 6087173.

ACCESSION AR103291

VERSION AR103291.1 GI:12814879
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., Ackermann,E.J. and Cowser,L.M.
TITLE Antisense modulation of X-linked inhibitor of apoptosis expression
JOURNAL Patent: US 6087173-A 11 11-JUL-2000;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCTTCTCTTGAAAATAGG 19
|||
Db 2 ATCTTCTCTTGAAAATAGG 20

RESULT 4

CQ890068

LOCUS CQ890068 33 bp DNA linear PAT 19-OCT-2004

DEFINITION Sequence 22 from Patent WO2004085660.

ACCESSION CQ890068

VERSION CQ890068.1 GI:54305762

KEYWORDS .

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE 1

AUTHORS Smith,J.F., Kamrud,K. and Rayner,J.O.

TITLE Improved alphavirus replicons and helper constructs

JOURNAL Patent: WO 2004085660-A 22 07-OCT-2004;

Alphavax, Inc. (US)

FEATURES Location/Qualifiers

source 1. .33

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="PCR primer"

ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCTTCTCTTGAAAATAGG 19
|||
Db 5 ATCTTCTCTTGAAAATAGG 23

RESULT 5

CS027754/c

LOCUS CS027754 19 bp RNA linear PAT 03-MAR-2005

DEFINITION Sequence 7 from Patent WO2005014811.

ACCESSION CS027754

VERSION CS027754.1 GI:60497304
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Mcswiggen,J. and Chowrira,B.M.
TITLE RNA interference mediated inhibition of XIAP gene expression using
short interfering Nucleic Acid (siNA)
JOURNAL Patent: WO 2005014811-A 7 17-FEB-2005;
Sirna Therapeutics, Inc. (US)
FEATURES Location/Qualifiers
source 1. .19
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Target
Sequence/siNA sense region"

ORIGIN

Query Match 94.7%; Score 18; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TCTTCTCTTGAAAATAGG 19
|||||||
Db 19 TCTTCTCTTGAAAATAGG 2

RESULT 6

CS028221

LOCUS CS028221 19 bp RNA linear PAT 03-MAR-2005

DEFINITION Sequence 474 from Patent WO2005014811.

ACCESSION CS028221

VERSION CS028221.1 GI:60497771

KEYWORDS .

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE 1

AUTHORS Mcswiggen,J. and Chowrira,B.M.

TITLE RNA interference mediated inhibition of XIAP gene expression using
short interfering Nucleic Acid (siNA)

JOURNAL Patent: WO 2005014811-A 474 17-FEB-2005;

Sirna Therapeutics, Inc. (US)

FEATURES Location/Qualifiers

source 1. .19

/organism="synthetic construct"

/mol_type="unassigned RNA"

/db_xref="taxon:32630"

/note="Description of Artificial Sequence: siNA antisense
region"

ORIGIN

Query Match 94.7%; Score 18; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TCTTCTCTTGAAAATAGG 19
|||||||
Db 1 TCTTCTCTTGAAAATAGG 18

RESULT 7

AR103290

LOCUS AR103290 20 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 10 from patent US 6087173.

ACCESSION AR103290

VERSION AR103290.1 GI:12814878

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 20)

AUTHORS Bennett,C.Frank., Ackermann,E.J. and Cowser,L.M.

TITLE Antisense modulation of X-linked inhibitor of apoptosis expression

JOURNAL Patent: US 6087173-A 10 11-JUL-2000;

FEATURES Location/Qualifiers

source 1. .20

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 94.7%; Score 18; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TCTTCTCTTGAAAATAGG 19

|||||

Db 1 TCTTCTCTTGAAAATAGG 18

RESULT 8

AR103292

LOCUS AR103292 20 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 12 from patent US 6087173.

ACCESSION AR103292

VERSION AR103292.1 GI:12814880

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 20)

AUTHORS Bennett,C.Frank., Ackermann,E.J. and Cowser,L.M.

TITLE Antisense modulation of X-linked inhibitor of apoptosis expression

JOURNAL Patent: US 6087173-A 12 11-JUL-2000;

FEATURES Location/Qualifiers

source 1. .20

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 89.5%; Score 17; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.2e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCTTCTCTTGAAAATA 17

|||||

Db 4 ATCTTCTCTTGAAAATA 20

RESULT 9

AR688306
LOCUS AR688306 50 bp DNA linear PAT 12-SEP-2005
DEFINITION Sequence 7735 from patent US 6905827.
ACCESSION AR688306
VERSION AR688306.1 GI:74470076
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Wohlgenuth,J., Fry,K., Woodward,R. and Ly,N.
TITLE Methods and compositions for diagnosing or monitoring auto immune
and chronic inflammatory diseases
JOURNAL Patent: US 6905827-A 7735 14-JUN-2005;
Expression Diagnostics, Inc.; So. San Francisco, CA
FEATURES Location/Qualifiers
source 1. .50
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 83.2%; Score 15.8; DB 2; Length 50;
Best Local Similarity 89.5%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATCTTCTCTTGAAAATAGG 19
||||| ||||||||| |||
Db 20 ATCTTTTCTTGAAAACAGG 38

RESULT 10

AR103293
LOCUS AR103293 20 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 13 from patent US 6087173.
ACCESSION AR103293
VERSION AR103293.1 GI:12814881
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., Ackermann,E.J. and Cowsert,L.M.
TITLE Antisense modulation of X-linked inhibitor of apoptosis expression
JOURNAL Patent: US 6087173-A 13 11-JUL-2000;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 78.9%; Score 15; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCTTCTCTTGAAAA 15
||||| |||||||||
Db 6 ATCTTCTCTTGAAAA 20

RESULT 11

CS249356/c

LOCUS CS249356 47 bp DNA linear PAT 18-JAN-2006
 DEFINITION Sequence 106 from Patent EP1614755.
 ACCESSION CS249356
 VERSION CS249356.1 GI:85361574
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Seibler, J.
 TITLE Target transgenesis of short hairpin RNA expression cassette using
 recombinase mediated cassette exchange
 JOURNAL Patent: EP 1614755-A 106 11-JAN-2006;
 ARTEMIS Pharmaceuticals GmbH (DE)
 FEATURES Location/Qualifiers
 source 1. .47
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Description of Artificial Sequence: DNA encoding an
 shRNA directed against the gene for the ubiquitin
 carboxyl-terminal hydrolase 20"

ORIGIN

Query Match 77.9%; Score 14.8; DB 2; Length 47;
 Best Local Similarity 88.9%; Pred. No. 6.3e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCTTCTCTTGAAAATAGG 19
 |||||
 Db 31 TCTTCTCTTGAAAGAAGG 14

RESULT 12

AR290347

LOCUS AR290347 47 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 2082 from patent US 6537751.
 ACCESSION AR290347
 VERSION AR290347.1 GI:31677631
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 47)
 AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
 TITLE Biallelic markers for use in constructing a high density
 disequilibrium map of the human genome
 JOURNAL Patent: US 6537751-A 2082 25-MAR-2003;
 Genset S.A.;;
 FRX;

FEATURES Location/Qualifiers
 source 1. .47
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 76.8%; Score 14.6; DB 2; Length 47;
 Best Local Similarity 93.3%; Pred. No. 8.1e+03;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCTCTTGAAAATAGG 19

Db |||||||:|||||
15 TCTCTTGAAMATAGG 29

RESULT 13

CQ550497/c

LOCUS CQ550497 60 bp DNA linear PAT 30-JAN-2004

DEFINITION Sequence 20132 from Patent WO0210449.

ACCESSION CQ550497

VERSION CQ550497.1 GI:41516924

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.

TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome

JOURNAL Patent: WO 0210449-A 20132 07-FEB-2002;
Compugen Inc. (US)

FEATURES

Location/Qualifiers

source 1. .60

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 75.8%; Score 14.4; DB 2; Length 60;

Best Local Similarity 93.8%; Pred. No. 1e+04;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TTCTCTTGAATAGG 19

|||||||:|||||

Db 36 TTCTCTTGAATTAGG 21

RESULT 14

CS249313/c

LOCUS CS249313 47 bp DNA linear PAT 18-JAN-2006

DEFINITION Sequence 63 from Patent EP1614755.

ACCESSION CS249313

VERSION CS249313.1 GI:85361531

KEYWORDS .

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE 1

AUTHORS Seibler,J.

TITLE Target transgenesis of short hairpin RNA expression cassette using
recombinase mediated cassette exchange

JOURNAL Patent: EP 1614755-A 63 11-JAN-2006;
ARTEMIS Pharmaceuticals GmbH (DE)

FEATURES

Location/Qualifiers

source 1. .47

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Description of Artificial Sequence: DNA encoding an
shRNA directed against the FLJ14914 (similar to UBP4)

gene"

ORIGIN

Query Match 74.7%; Score 14.2; DB 2; Length 47;
 Best Local Similarity 84.2%; Pred. No. 1.4e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATCTTCTCTTGAAAATAGG 19
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 Db 32 ATCTTCTCTTGAAAGATGG 14

RESULT 15

CQ544851

LOCUS CQ544851 60 bp DNA linear PAT 30-JAN-2004

DEFINITION Sequence 14486 from Patent WO0210449.

ACCESSION CQ544851

VERSION CQ544851.1 GI:41511115

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1

AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.

TITLE Oligonucleotide library for detecting rna transcripts and splice
 variants that populate a transcriptome

JOURNAL Patent: WO 0210449-A 14486 07-FEB-2002;
 Compugen Inc. (US)

FEATURES Location/Qualifiers

source 1. .60
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 74.7%; Score 14.2; DB 2; Length 60;
 Best Local Similarity 84.2%; Pred. No. 1.3e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATCTTCTCTTGAAAATAGG 19
 |||||
 Db 35 ATCTTCTGTGAAAATGGG 53

RESULT 16

A42870

LOCUS A42870 69 bp DNA linear PAT 06-MAR-1997

DEFINITION Sequence 2 from Patent WO9502701.

ACCESSION A42870

VERSION A42870.1 GI:2298319

KEYWORDS

SOURCE unidentified

ORGANISM unidentified

unclassified sequences.

REFERENCE 1 (bases 1 to 69)

AUTHORS Abken,H.J., Albert,W. and Jungfer,H.

TITLE METHOD OF IDENTIFYING HUMAN AND ANIMAL CELLS CAPABLE OF UNLIMITED
 PROLIFERATION OR TUMOUR FORMATION

JOURNAL Patent: WO 9502701-A 2 26-JAN-1995;

BOEHRINGER MANNHEIM GMBH (DE)
COMMENT Other publication DE 4323727 950309.
FEATURES Location/Qualifiers
source 1. .69
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 74.7%; Score 14.2; DB 2; Length 69;
Best Local Similarity 84.2%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATCTTCTCTTGAAAATAGG 19
||||| ||||| ||
Db 2 ATCTTTTCTTGAAAGTACG 20

RESULT 17

AR271404

LOCUS AR271404 69 bp DNA linear PAT 10-APR-2003

DEFINITION Sequence 2 from patent US 6503706.

ACCESSION AR271404

VERSION AR271404.1 GI:29702822

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 69)

AUTHORS Abken,H.J., Albert,W. and Jungfer,H.

TITLE Method for identifying human and animal cells having an unlimited proliferation of tumor-formation potential

JOURNAL Patent: US 6503706-A 2 07-JAN-2003;
Roche Diagnostics GmbH; Mannheim;
DEX;

FEATURES Location/Qualifiers
source 1. .69.
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 74.7%; Score 14.2; DB 2; Length 69;
Best Local Similarity 84.2%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATCTTCTCTTGAAAATAGG 19
||||| ||||| ||
Db 2 ATCTTTTCTTGAAAGTACG 20

RESULT 18

CS174292/c

LOCUS CS174292 47 bp DNA linear PAT 12-OCT-2005

DEFINITION Sequence 56 from Patent WO2005090603.

ACCESSION CS174292

VERSION CS174292.1 GI:77625158

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE 1

AUTHORS Nakamura, Y.
TITLE Method for diagnosing non-small cell lung cancer
JOURNAL Patent: WO 2005090603-A 56 29-SEP-2005;
The University of Tokyo (JP); Oncotherapy Science, Inc. (JP)
FEATURES Location/Qualifiers
source 1. 47
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="An artificially synthesized oligonucleotide
sequence for hairpin siRNA"

ORIGIN

Query Match 73.7%; Score 14; DB 2; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCTTCTCTTGAAA 14
|||||||
Db 32 ATCTTCTCTTGAAA 19

RESULT 19

CS174290/c
LOCUS CS174290 51 bp DNA linear PAT 12-OCT-2005

DEFINITION Sequence 54 from Patent WO2005090603.

ACCESSION CS174290

VERSION CS174290.1 GI:77625156

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1

AUTHORS Nakamura, Y.

TITLE Method for diagnosing non-small cell lung cancer

JOURNAL Patent: WO 2005090603-A 54 29-SEP-2005;

The University of Tokyo (JP); Oncotherapy Science, Inc. (JP)

FEATURES Location/Qualifiers

source 1. 51
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="An artificially synthesized oligonucleotide
sequence for construction of siRNA expression vector"

ORIGIN

Query Match 73.7%; Score 14; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCTTCTCTTGAAA 14
|||||||
Db 36 ATCTTCTCTTGAAA 23

RESULT 20

CS174291
LOCUS CS174291 51 bp DNA linear PAT 12-OCT-2005

DEFINITION Sequence 55 from Patent WO2005090603.

ACCESSION CS174291

VERSION CS174291.1 GI:77625157

KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE

1
AUTHORS Nakamura, Y.
TITLE Method for diagnosing non-small cell lung cancer
JOURNAL Patent: WO 2005090603-A 55 29-SEP-2005;
The University of Tokyo (JP); Oncotherapy Science, Inc. (JP)

FEATURES

Location/Qualifiers
source 1. .51
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="An artificially synthesized oligonucleotide
sequence for construction of siRNA expression vector"

ORIGIN

Query Match 73.7%; Score 14; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCTTCTCTTGAAA 14
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Db 20 ATCTTCTCTTGAAA 33

RESULT 21

CQ550203/c

LOCUS CQ550203 60 bp DNA linear PAT 30-JAN-2004

DEFINITION Sequence 19838 from Patent WO0210449.

ACCESSION CQ550203

VERSION CQ550203.1 GI:41516630

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1
AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 19838 07-FEB-2002;
Compugen Inc. (US)

FEATURES

Location/Qualifiers
source 1. .60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 73.7%; Score 14; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCTTCTCTTGAAA 14
|||||
Db 25 ATCTTCTCTTGAAA 12

RESULT 22

AX516067

LOCUS AX516067 41 bp DNA linear PAT 05-OCT-2002

DEFINITION Sequence 2265 from Patent WO02052044.

ACCESSION AX516067

VERSION AX516067.1 GI:23563647

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.

TITLE Detection of genetic polymorphisms

JOURNAL Patent: WO 02052044-A 2265 04-JUL-2002;
Riken (JP)

FEATURES Location/Qualifiers

source 1..41

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

misc_feature 21

/note="n represents tt or deletion"

ORIGIN

Query Match 72.6%; Score 13.8; DB 2; Length 41;

Best Local Similarity 83.3%; Pred. No. 2.3e+04;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCTTCTCTTGAAAATAG 18

||||| ||| |||

Db 11 ATCTTCTCTCNAACTAG 28

RESULT 23

AX517473

LOCUS AX517473 41 bp DNA linear PAT 05-OCT-2002

DEFINITION Sequence 3671 from Patent WO02052044.

ACCESSION AX517473

VERSION AX517473.1 GI:23566100

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.

TITLE Detection of genetic polymorphisms

JOURNAL Patent: WO 02052044-A 3671 04-JUL-2002;
Riken (JP)

FEATURES Location/Qualifiers

source 1..41

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 72.6%; Score 13.8; DB 2; Length 41;

Best Local Similarity 83.3%; Pred. No. 2.3e+04;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATCTTCTCTTGAAAATAG 18
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 Db 11 ATCTTCTCTCNAACTAG 28

RESULT 24

AX520878

LOCUS AX520878 41 bp DNA linear PAT 05-OCT-2002

DEFINITION Sequence 7076 from Patent WO02052044.

ACCESSION AX520878

VERSION AX520878.1 GI:23571558

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1

AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.

TITLE Detection of genetic polymorphisms

JOURNAL Patent: WO 02052044-A 7076 04-JUL-2002;
 Riken (JP)

FEATURES

Location/Qualifiers

source

1. .41

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 72.6%; Score 13.8; DB 2; Length 41;

Best Local Similarity 88.2%; Pred. No. 2.3e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATCTTCTCTTGAAAATA 17
 ||||| |||||
 Db 25 ATCTTGTTTTGAAAATA 41

RESULT 25

AR290700

LOCUS AR290700 47 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 2435 from patent US 6537751.

ACCESSION AR290700

VERSION AR290700.1 GI:31677984

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 47)

AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.

TITLE Biallelic markers for use in constructing a high density
 disequilibrium map of the human genomeJOURNAL Patent: US 6537751-A 2435 25-MAR-2003;
 Genset S.A.;;

FRX;

FEATURES

Location/Qualifiers

source

1. .47

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 72.6%; Score 13.8; DB 2; Length 47;
Best Local Similarity 88.2%; Pred. No. 2.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATCTTCTCTTGAAAATA 17
 .|| || |||||
 Db 6 ATTTTATCTTGAAAATA 22

RESULT 26

CS048040/c

LOCUS CS048040 51 bp DNA linear PAT 22-MAR-2005

DEFINITION Sequence 83 from Patent WO2005019475.

ACCESSION CS048040

VERSION CS048040.1 GI:61853734

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE

AUTHORS Nakamura, Y. and Katagiri, T.

TITLE Hypoxia-inducible protein 2 (hig2), a novel therapeutic potentialtarget of renal cell carcinoma (rcc)

JOURNAL Patent: WO 2005019475-A 83 03-MAR-2005;
Oncotherapy Science, Inc. (JP); The University of Tokyo (JP)

FEATURES

Location/Qualifiers

source

1. 51 .

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/organism="synthetic construct"
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/mol type="unassigned DNA"
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/db xref="taxon:32630"
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/note="an artificially synthesized oligonucleotide
sequence for siRNA"
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ORIGIN

Query Match 72.6%; Score 13.8; DB 2; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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SCORE 1.3 BuildDate: 11/17/2006